

Serial No. 09/486,334
Atty No. 5500*42

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of claims

Claims 1-5 (canceled)

Claim 6 (currently amended): The method according to claim 78 ~~claim 60~~, wherein the serine acetyltransferase is overexpressed in the cytoplasm of plant cells.

Claims 7 and 8. (canceled)

Claim 9 (currently amended): The method according to claim 62, wherein the serine acetyltransferase is SAT3, which ~~SAT3~~ is represented by SEQ ID NO: 2.

Claim 10 (withdrawn): Method according to claim 6, characterized in that the SAT is a non-cytoplasmic plant SAT from which has been removed its signal(s) for addressing to cellular compartments other than the cytoplasm.

Claim 11 (withdrawn): Method according to claim 10, characterized in that the SAT is SAT1' which is represented by SEQ ID NO 2.

Claims 12-14 (canceled)

Claim 15 (withdrawn): Method according to claim 13, characterized in that the SAT is a mitochondrial SAT of plant origin, in particular from *Arabidopsis thaliana*.

Claim 16 (withdrawn): Method according to claim 15, characterized in that the SAT is SAT1 which is represented by SEQ ID NO 3.

Claim 17 (currently amended): The method according to claim 78 ~~claim 60~~, wherein the serine acetyltransferase is overexpressed in chloroplasts of plant cells.

Claim 18 (currently amended): The method according to claim 17, wherein the serine acetyltransferase is overexpressed in chloroplasts by integration, into chloroplast DNA of plant cells, of a chimeric gene comprising a DNA sequence encoding the serine acetyltransferase, wherein said DNA sequence is under the control of 5' and 3' regulatory elements which are functional in chloroplasts.

Claim 19 (previously amended): The method according to claim 17, wherein the serine

acetyltransferase is overexpressed in the cytoplasm in the form of a transit peptide/ serine acetyltransferase fusion protein, wherein the mature functional serine acetyltransferase is released inside the chloroplasts.

Claim 20 (previously amended): The method according to claim 19, wherein the serine acetyltransferase and transit peptide of the fusion protein are from the same protein.

Claim 21 (withdrawn): Method according to claim 20, characterized in that the SAT is a chloroplast SAT of plant origin, in particular from *Arabidopsis thaliana*.

Claim 22 (withdrawn): Method according to claim 21, characterized in that the SAT is SAT2 or SAT4 which are represented by SEQ ID NO 5 or NO 6, respectively.

Claim 23 (previously amended): The method according to claim 19, wherein the serine acetyltransferase and the transit peptide of the fusion protein are from different proteins.

Claim 24 (canceled).

Claim 25 (previously amended): The method according to claim 23, wherein the transit peptide is a transit peptide from a plastid protein other than a chloroplast serine acetyltransferase.

Claim 26 (previously amended): The method according to claim 25, wherein the transit peptide consists of a plant EPSPS transit peptide or a plant RuBisCO ssu transit peptide.

Claims 27-30 (canceled).

Claim 31 (withdrawn): Transit peptide/SAT fusion protein, characterized in that the SAT is heterologous with the transit peptide.

Claim 32 (withdrawn): Fusion protein according to claim 31, characterized in that the SAT is a cytoplasmic SAT of plant origin or an SAT of bacterial origin, and that the SAT is a plant SAT or a native SAT of bacterial origin.

Claim 33 (withdrawn): Nucleic acid sequence encoding a transit peptide/SAT fusion protein according to claim 31.

Claim 34 (withdrawn): Chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, characterized in that the coding sequence comprises at least one nucleic acid sequence which

encodes an SAT.

Claim 35 (withdrawn): Chimeric gene according to claim 34, characterized in that the host organism is chosen from bacteria, for example *E. coli*, yeasts, in particular of the genera *Saccharomyces*, *Kluyveromyces* or *Pichia*, fungi, in particular Aspergillus, baculoviruses, or plant cells and plants.

Claim 36 (withdrawn): Chimeric gene according to claim 35, characterized in that the host organism is a plant cell or a plant which contains it.

Claim 37 (withdrawn): Chimeric gene according to claim 36, characterized in that the 5' regulatory element comprises regulatory sequences which are promoters in plant cells and plants, and are chosen from promoters which are expressed in plant leaves, constitutive promoters, or light-dependent promoters of bacterial, viral or plant origin.

Claim 38 (withdrawn): Chimeric gene according to claim 36, characterized in that the 5' regulatory element comprises regulatory sequences which are promoters in plant cells and plants, and are chosen from seed-specific promoters.

Claim 39 (withdrawn): Chimeric gene according to claim 38, characterized in that the promoter is chosen from the promoters for napin, phaseolin, glutein, zein, helianthinin, albumin and oleosin.

Claim 40 (withdrawn): Chimeric gene according to claim 34, characterized in that the nucleic acid sequence which encodes an SAT encodes an SAT in that the SAT which is overexpressed in plant cells is a cysteine-sensitive SAT.

Claim 41 (withdrawn): Chimeric gene according to claim 34, characterized in that the nucleic acid sequence which encodes an SAT is the nucleic acid sequence encoding a transit peptide/SAT fusion protein and that the SAT is heterologous with the transit peptide.

Claim 42 (withdrawn): Cloning and/or expression vector for transforming a host organism, characterized in that it contains at least one chimeric gene as defined according to claim 34.

Claim 43 (withdrawn): Method of transforming host organisms, characterized in that at

least one nucleic acid sequence according to claim 33, or a chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, and that the coding sequence comprises at least one nucleic acid sequence which encodes an SAT, is integrated into the genome of the said host organism.

Claim 44 (withdrawn): Method according to claim 43, by means of the vector for transforming a host organism, characterized in that it contains at least one chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, and that the coding sequence comprises at least one nucleic acid sequence which encodes an SAT.

Claim 45 (withdrawn): Method according to claim 43, characterized in that the host organism is chosen from bacteria, for example *E. coli*, yeasts, in particular of the genera *Saccharomyces*, *Kluyveromyces* or *Pichia*, fungi, in particular *Aspergillus*, baculoviruses, or plant cells and plants.

Claim 46 (withdrawn): Method according to claim 45, characterized in that the host organism is a plant cell or a plant which contains it.

Claim 47 (withdrawn): Method according to claim 46, characterized in that the plant is regenerated from a transformed plant cell.

Claim 48 (withdrawn): Method according to claim 47, characterized in that the host organism is a monocotyledonous plant, in particular chosen from cereals, sugar cane, rice and maize, or a dicotyledonous plant, in particular chosen from tobacco, soybean, rape, cotton, beet and clover.

Claim 49 (withdrawn): Transformed host organism, characterized in that it comprises at least one nucleic acid sequence according to claim 33, or a chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, and that the coding sequence comprises at least one nucleic acid sequence which encodes an SAT.

Claim 50 (withdrawn): Host organism according to claim 49, characterized in that it is

obtained by the method of transforming host organisms, characterized in that at least one nucleic acid sequence encoding a transit peptide/SAT fusion protein, characterized in that the SAT is heterologous with the transit peptide, or a chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, and that the coding sequence comprises at least one nucleic acid sequence which encodes an SAT, is integrated into the genome of the said host organism.

Claim 51 (withdrawn): Plant cell, characterized in that it comprises at least one nucleic acid sequence according to claim 33, or a chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, characterized in that the coding sequence comprises at least one nucleic acid sequence which encodes an SAT.

Claim 52 (withdrawn): Genetically modified plant, characterized in that it comprises at least one plant cell according to claim 51.

Claim 53 (withdrawn): Plant according to claim 52, characterized in that the plant is regenerated from a plant cell and that it comprises at least one nucleic acid sequence encoding a transit peptide/SAT fusion protein, characterized in that the SAT is heterologous with the transit peptide.

Claim 54 (withdrawn): Genetically modified plant, characterized in that it is derived from the culture and/or crossing of regenerated plants, according to claim 53.

Claim 55 (withdrawn): Genetically modified plant according to claim 52, characterized in that it is a monocotyledonous plant, in particular chosen from cereals, sugar cane, rice and maize, or a dicotyledonous plant, in particular chosen from tobacco, soybean, rape, cotton, beet and clover.

Claim 56 (withdrawn): Genetically modified plant according to claim 52, characterized in that it comprises other genes of interest.

Claim 57 (withdrawn): Genetically modified plant according to claim 56, characterized in that it comprises at least one other gene which modifies the content and quality of the proteins

Serial No. 09/486,334

Atty No. 5500*42

of the said plant, in particular in the leaves and/or seeds.

Claim 58 (withdrawn): Genetically modified plant according to claim 56, characterized in that the gene encodes a protein enriched in sulphur-containing amino acids.

Claim 59 (withdrawn): Seeds of genetically modified plants according to claim 52.

Claim 60 (canceled).

Claim 61 (previously amended): The method of claim 6, wherein the serine acetyltransferase is a plant cytoplasmic serine acetyltransferase.

Claim 62 (previously amended): The method of claim 61, wherein the plant cytoplasmic serine acetyltransferase is from *Arabidopsis thaliana*.

Claims 63 and 64 (canceled).

Claim 65 (previously amended): The method of claim 19, wherein said serine acetyltransferase is a plant cytoplasmic serine acetyltransferase or a bacterial serine acetyltransferase.

Claims 66-69 (canceled).

Claim 70 (previously amended): The method of claim 25, wherein said transit peptide comprises a plant plastid transit peptide, an N-terminal portion of a mature plastid protein linked by its N-terminus to the C-terminus of said plastid transit peptide, and a second plastid transit peptide linked by its N-terminus to the C-terminus of said N-terminal portion of a mature plastid protein.

Claim 71 (currently amended): The method of claim 70, wherein said transit peptide is an optimized transit peptide (OTP) comprised of the sunflower RuBisCO ssu transit peptide fused to a peptide made of the twenty-two N-terminal amino acids of the mature maize RuBisCO ssu, which is in turn fused to the ~~to the~~ maize RuBisCO ssu transit peptide.

Claims 72 and 73 (canceled).

Claim 74 (canceled).

Claim 75 (currently amended): The method of claim 79 ~~claim 74~~, wherein said nucleotide sequence encodes SAT3, ~~which~~ SAT3 ~~which~~ is represented by SEQ ID NO: 2.

Claim 76 (canceled).

Claim 77 (currently amended): The method of claim 80 ~~claim 76~~ wherein said nucleotide sequence encodes SAT3, which ~~SAT3~~ which is represented by SEQ ID NO: 2.

Claim 78 (new): A method for increasing the production of cysteine, glutathione, methionine or sulfur-containing derivatives of methionine by plant cells, said method consisting of

transforming plant cells with a nucleic acid sequence encoding a cysteine-insensitive serine acetyltransferase; and

optionally regenerating a transformed plant from said transformed plant cells,

whereby said transformed plant cells overexpress, or optionally said transformed plant overexpresses, serine acetyltransferase resulting in an increase in production of cysteine, glutathione, methionine, or sulfur-containing derivatives of methionine by said transformed plant cells or plant in comparison with the level observed in nontransformed plant cells or plant of the same type as said transformed cells or plant.

Claim 79 (new): A method for increasing the production of cysteine, glutathione, methionine or sulfur-containing derivatives of methionine by plant cells, said method consisting of

culturing plant cells transformed with a nucleic acid sequence encoding a cysteine-insensitive serine acetyltransferase;

whereby said transformed plant cells overexpress serine acetyltransferase resulting in an increase in production of cysteine, glutathione, methionine, or sulfur-containing derivatives of methionine by said transformed plant cells in comparison with the level observed in nontransformed plant cells of the same type as said transformed plant cells.

Claim 80 (new): A method for increasing the production of cysteine, glutathione, methionine or sulfur-containing derivatives of methionine by a plant, said method consisting of

culturing plant cells transformed with a nucleic acid sequence encoding a cysteine-insensitive serine acetyltransferase; and

Serial No. 09/486,334

Atty No. 5500*42

regenerating a transformed plant from said transformed plant cells,
whereby said transformed plant overexpresses serine acetyltransferase resulting in an
increase in production of cysteine, glutathione, methionine, or sulfur-containing derivatives of
methionine by said transformed plant in comparison with the level observed in a nontransformed
plant of the same type as said transformed plant.